

TITLE Danielenko, D.M.
FGF-18, a novel member of the fibroblast growth factor family,
stimulates hepatic and intestinal proliferation
JOURNAL Mol. Cell. Biol. 18 (10), 6063-6074 (1998)
MEDLINE 98414622
PUBMED 9742123
REFERENCE 2 (bases 1 to 1546)
AUTHORS Hu, M.C.-T.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1998) Departments of Cell Biology, Amgen, Inc.,
One Amgen Center, 14-1-D, Thousand Oaks, CA 91320, USA

FEATURES

source 1..1546
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..1546
/gene="FGF18"
538..1161
/gene="FGF18"
/function="stimulates hepatic and intestinal
proliferation"
/note="FGF-18"
/codon_start=1
/product="fibroblast growth factor 18"
/protein_id="AAC62240.1"
/db_xref="GI:3687843"
/translation="MSAPSACTCLCLHFLLCFOVQLVAENYDFRIHVENQTRAR
DVSRSKQLYOLYRSKSHIYQVLRIRISARGEDBDKRAQLVETDFGSOVKIKG
EFPEYLCKMRKSLVGRKPDGTSKECFIEKVFLENNYTAAMSKEYSWYGFTRKGGPR
KGPRTRENDQDVHFMKRYRKPQDPELOKPRKYTYTVIKRSRIRPTHPA"

BASE COUNT 360 a 482 c 486 g 218 t
ORIGIN

Query Match 97.4%; Score 1528.8; DB 9; Length 1546;
Best Local Similarity 99.5%; Pred. No. 5.2e-241;
Matches 1533; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 19 CGTGGGAGCGGAGAGAGACATGAGCGCGGCGCCAGAGAGCGCGCTGACG 78
DB 7 CGAGAGAGCGCGGAGAGAGACATGAGCGCGGCGCCAGAGAGCGCGCTGACG 66
QY 79 CTTTGGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 138
DB 67 CTTTGGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
QY 139 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 198
DB 127 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
QY 199 ACTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 258
DB 187 ACTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
QY 259 GAGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 318
DB 247 GAGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 306
QY 319 GCCAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 378
DB 307 GCCAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366
QY 379 CGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 438
DB 367 CGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 426
QY 439 AGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 498
DB 427 AGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 486
QY 499 GCGGACATGTGAGCGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
DB 487 GCGGACATGTGAGCGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546

QY 559 GCGCCCTCGCGCTGCACCTGCTGTGTTACATCTCCCTGCTGTGCTTCCAGTACG 618
DB 547 GCGCCCTCGCGCTGCACCTGCTGTGTTACATCTCCCTGCTGTGCTTCCAGTACG 606
QY 619 GTGCTGTTGCGCAGAGAAAGTGGCTTCCGATCCAGTGGAGAAACAGAGCGGGCT 678
DB 607 GTGCTGTTGCGCAGAGAAAGTGGCTTCCGATCCAGTGGAGAAACAGAGCGGGCT 666
QY 679 CGGAGAGTGTGAGCGGTAAAGAGAGTGGCTTACAGCTTACAGCGCGGAGTGGG 738
DB 667 CGGAGAGTGTGAGCGGTAAAGAGAGTGGCTTACAGCTTACAGCGCGGAGTGGG 726
QY 739 AAACATCCAGTCTCGGGCGCGAGATGATGCGCGCGGAGAGTGGGCAAGTAT 798
DB 727 AAACATCCAGTCTCGGGCGCGAGATGATGCGCGCGGAGAGTGGGCAAGTAT 786
QY 799 GCCAGCTCTAGTGGAGAGACACCTTGGTGAAGTCCGGATCCAGGCAAGGAGAG 858
DB 787 GCCAGCTCTAGTGGAGAGACACCTTGGTGAAGTCCGGATCCAGGCAAGGAGAG 846
QY 859 ACGGAATTCATCTGTGATGAACCGCAAGCAAGCTGTGGGAGAGCGGATGGCACC 918
DB 847 ACGGAATTCATCTGTGATGAACCGCAAGCAAGCTGTGGGAGAGCGGATGGCACC 906
QY 919 AGCAAGAGTGTGTTCATCGAAGAGTTCGGAACAACATCAAGCGGCTGATGTG 978
DB 907 AGCAAGAGTGTGTTCATCGAAGAGTTCGGAACAACATCAAGCGGCTGATGTG 966
QY 979 GCTAAGTACCTCGCGTGTGATGAGTGGCTTACCAGAGAGGCGCGCGGAGAGGCGCC 1038
DB 967 GCTAAGTACCTCGCGTGTGATGAGTGGCTTACCAGAGAGGCGCGCGGAGAGGCGCC 1026
QY 1039 AAGACCGGAGAGAACAGAGAGAGTGCATTTTCATGAAGCGTACCCCAAGGGCGACGCC 1098
DB 1027 AAGACCGGAGAGAACAGAGAGAGTGCATTTTCATGAAGCGTACCCCAAGGGCGACGCC 1086
QY 1099 GAGCTTCAGAGCGCTTCATGAATACAGAGGTGACCAAGAGTCCGTGATCGGCGCC 1158
DB 1087 GAGCTTCAGAGCGCTTCATGAATACAGAGGTGACCAAGAGTCCGTGATCGGCGCC 1146
QY 1159 ACACACCGTGTGAGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1218
DB 1147 ACACACCGTGTGAGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1206
QY 1219 TCCAGAGAAAGTGCATCAGAGAGAAATTTTTCATGAAGAAATTAAGAGAAAGCTATTT 1278
DB 1207 TCCAGAGAAAGTGCATCAGAGAGAAATTTTTCATGAAGAAATTAAGAGAAAGCTATTT 1266
QY 1279 TTGTACATTTGTGTTAAAGAGAGCAAAACTGAACCAAAACTTTGGGGAGAGGGTGA 1338
DB 1267 TTGTACATTTGTGTTAAAGAGAGCAAAACTGAACCAAAACTTTGGGGAGAGGGTGA 1326
QY 1339 TTAAGATTTTATTTGATGAATGAACCGCGGATGAACCAAGACTGACGAAGGAGCTGT 1398
DB 1327 TTAAGATTTTATTTGATGAATGAACCGCGGATGAACCAAGACTGACGAAGGAGCTGT 1386
QY 1399 AGTCAACCCACAGAGTGTGTCTCTCTAGAGAACAGACAATCTTAACTCTCCACAGA 1458
DB 1387 AGTCAACCCACAGAGTGTGTCTCTCTAGAGAACAGACAATCTTAACTCTCCACAGA 1446
QY 1459 GGAAGCATTTGAATGAGAGAAACCAACACTTTGAGAAAGCCAAAGTCTTTTCCAAAGGTT 1518
DB 1447 GGAAGCATTTGAATGAGAGAAACCAACACTTTGAGAAAGCCAAAGTCTTTTCCAAAGGTT 1506
QY 1519 CTGAAGAGGAAAAAACAACAAAAAACAACAAAAAACAACAAAAAACAACAAAAA 1558
DB 1507 CTGAAGAGGAAAAAACAACAAAAAACAACAAAAAACAACAAAAAACAACAAAAA 1546

RESULT 2
LOCUS BC006245 1163 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, fibroblast growth factor 18, clone MGC:10529

RESULT 3
AX427499 1517 bp DNA linear PAT 20-JUN-2002
LOCUS AX427499
DEFINITION Sequence 9 from Patent WO0121836.
ACCESSION AX427499
VERSION AX427499.1 GI:21537645
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
Bratcher, Shawn,R., Dufour,G.F., Cohen,H.J., Rosen,B.H., Shah,P.,
Chalup,M.S., Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B.,
Panzer,S.R., Roseberry,A.M., Wright,R.J., Chen,W., Liu,T.,
Yap,P.E., Stockdreher,T.K., Amshy,S. and Pong,W.T.
TITLE Molecules for diagnostics and therapeutics
JOURNAL Patent: WO 0121836-A 9 29-MAR-2001;
Incyle Genomics, Inc. (US)
FEATURES
source 1. 1517
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyle ID No: 237152.1.dec"
BASE COUNT 419 a 424 c 370 g 302 t 2 others
ORIGIN
Query Match 68.0%; Score 1068; DB 6; Length 1517;
Best Local Similarity 98.9%; Pred. No. 1.9e-165;
Matches 1074; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 483 GTCCCGCGCGCGGAGGAGGAGCATGTGAGGCTGGGCTAGAGCCGCGCTCCCTCCG 542
DB 1 GTCCCGCGCGCGGAGGAGGAGCATGTGAGGCTGGGCTAGAGCCGCGCTCCCTCCG 60
QY 543 CCCAGCATGATTATAGCGCCCTCCGCTGACATTGCTGTATACACTTCTCTGCT 602
DB 61 CCCAGCATGATTATAGCGCCCTCCGCTGACATTGCTGTATACACTTCTCTGCT 120
QY 603 GTGCTCCAGGTACAGTGTGCTGTGGCGAGAGAAAGTGAGCTCCGATCCAGTGGGA 662
DB 121 GTGCTCCAGGTACAGTGTGCTGTGGCGAGAGAAAGTGAGCTCCGATCCAGTGGGA 180
QY 663 GAACCAAGCGGCGCTCGGAGATGTAGCCGTAAAGCAGCTGCGCTGTACACCTCTA 722
DB 181 GAACCAAGCGGCGCTCGGAGATGTAGCCGTAAAGCAGCTGCGCTGTACACCTCTA 240
QY 723 CAGCGGACCAAGTGGGAAACATCCAGAGTCTGGGCGGAGATCAGTCCCGCGGCGA 782
DB 241 CAGCGGACCAAGTGGGAAACATCCAGAGTCTGGGCGGAGATCAGTCCCGCGGCGA 300
QY 783 GGATGGGACAGTATGCGCAGCTCTAGTGGAGACACACCTCGGTAGACAGTCCG 842
DB 301 GGATGGGACAGTATGCGCAGCTCTAGTGGAGACACACCTCGGTAGACAGTCCG 360
QY 843 GATCAAGGGCAAGAGAGCAATTCCTGTGATGAAACCGCAAGCAAGCTGTGGG 902
DB 361 GATCAAGGGCAAGAGAGCAATTCCTGTGATGAAACCGCAAGCAAGCTGTGGG 420
QY 903 GAAGCCCATGGCACCAAGAGAGTGTGTTCATCGAAGAGTTCTGAGAACACTA 962
DB 421 GAAGCCCATGGCACCAAGAGAGTGTGTTCATCGAAGAGTTCTGAGAACACTA 480
QY 963 CAGCGCCCTGATGCGGTAGTACTCGGCTGGTATGAGTGGGCTTCACCAAGAGGGCG 1022
DB 481 CAGCGCCCTGATGCGGTAGTACTCGGCTGGTATGAGTGGGCTTCACCAAGAGGGCG 540
QY 1023 GCCCGGAAAGGGCCCAAGACCCGGAGAACACAGCAGAGCTGATTTTCATGAAGCGCTA 1082
DB 541 GCCCGGAAAGGGCCCAAGACCCGGAGAACACAGCAGAGCTGATTTTCATGAAGCGCTA 600
QY 1083 CCCCAAGGGGCGAGCGGAGCTTCAGAAAGCCTTCAAGTACAGACGCGTGACCAAGAGGTC 1142

DB 601 CCCCAAGGGGCGAGCGGAGCTTCAGAAAGCCTTCAAGTACAGACGCTTACCAGAGGTC 660
QY 1143 CCGTGCATCCGCGCCACACACACCTTCGCTAGGCGCACCCCGCGGCGCTCAGGTCGCG 1202
DB 661 CCGTGCATCCGCGCCACACACCTTCGCTAGGCGCACCCCGCGGCGCTCAGGTCGCG 720
QY 1203 CTGGCCACATCAGACCTCCAGAAAACATCAGAGAAATATTTTACATGAAAAATTA 1262
DB 721 CTGGCCACATCAGACCTCCAGAAAACATCAGAGAAATATTTTACATGAAAAATTA 780
QY 1263 GGAAGAGCTCTATTTTGTATCTGTGTAAAGAGACAAAACCTAACCAAACTC 1322
DB 781 GGAAGAGCTCTATTTTGTATCTGTGTAAAGAGACAAAACCTAACCAAACTC 840
QY 1323 TTGGGGGGGGGGGTAGTAAGATTTATTTGACTTGAACCCCGATGACAAAAGACT 1382
DB 841 TTGGGGGGGGGGGTAGTAAGATTTATTTGACTTGAACCCCGATGACAAAAGACT 900
QY 1383 CAGCAAAAGGAGCTAGTCAACCCACAGCTGCTCTCTCTAGAACAGACACTC 1442
DB 901 CAGCAAAAGGAGCTAGTCAACCCACAGCTGCTCTCTCTCTAGAACAGACACTC 960
QY 1443 TAACTCTGTCGCCAGAGAGACTTGATGAGAAAACCAACTTTGAGACCAAGTC 1502
DB 961 TAACTCTGTCGCCAGAGAGACTTGATGAGAAAACCAACTTTGAGACCAAGTC 1020
QY 1503 CTTTTCCCAAGGTTTCGAAAGAAAAAACAACAAAAAAGAAAAAAGAAAAA 1562
DB 1021 CTTTTCCCAAGGTTTCGAAAGAAAAAACAACAAAAAAGAAAAAAGAAAAA 1080
QY 1563 AAAAAA 1568
DB 1081 GAGAAA 1086
RESULT 4
AF075291 1094 bp mRNA linear ROD 02-OCT-1998
LOCUS AF075291
DEFINITION Mus musculus fibroblast growth factor 18 (Fgf18) mRNA, complete
cde
ACCESSION AF075291
VERSION AF075291.1 GI:3687840
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1094)
AUTHORS Hu,M.C.-T., Qiu,W.R., Wang,Y.-P., Hill,D., Ring,B.D., Scully,S.,
Bolton,B., DeRose,M., Luethy,R., Simonet,W.S., Arakawa,T. and
Danilenko,D.M.
TITLE FGF-18, a novel member of the fibroblast growth factor family,
stimulates hepatic and intestinal proliferation
JOURNAL Mol. Cell. Biol. 18 (10), 6063-6074 (1998)
MEDLINE 98414622
PUBMED 9742123
REFERENCE 2 (bases 1 to 1094)
AUTHORS Hu,M.C.-T.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1998) Departments of Cell Biology, Amgen, Inc.,
One Angen Center, 14-1-D, Thousand Oaks, CA 91320, USA
FEATURES
source 1. 1094
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
1. 1094
/gene="Fgf18"
136..759
/gene="Fgf18"
/function="stimulates hepatic and intestinal
proliferation"
/note="Fgf-18"

```

/codon_start=1
/product="fibroblast growth factor 18"
/protein_id="AAC62239.1"
/db_xref="GI:3687841"
/translation="MYSAPSACCTCLCHPLLCLFOYVLAEEVDFRIHVENOTRAR
DVSRSKRLRRLQYVSPFGKHIOVLGRISVARGSDGKVLQOLVETDFPSOYAIK
KEEFLYCLMNRGKLVGKPDGTSKECVILEVLVLEVALMSAYSGVYVFTKKGRR
KGGKTRRNQDDVHFMRKRYPRGQAEHLQPEFYITVTYKNSRRIRPThpG"
BASE COUNT      287 a      301 c      315 g      191 t
ORIGIN

```

Query Match	52.1%;	Score 818.6;	DB 10;	Length 1094;
Best Local Similarity	87.3%;	Pred. No. 1.4e-124;		
Matches 980; Conservative	0;	Mismatches 104;	Indels 39;	Gaps 6

[illegible]

Db	822	GGAGAAATCTCATTTTTGTACATGTGTAAAAAGAGACAAAACAGTAACCTPAAAGTC	881
Oy	1323	TTGGGGGGGAGGGGATGAAGATTTTATGTGTACTTAAACCCCGATGACAAAAGACT	1382
Db	882	TTGGGAGGAGGGGGCGCAT -AGATTTTCCACTGTTGACCTGAA-- -GCCCATGTCAAAAGACT	937
Oy	1383	CACGCAAGGGAGCTGTACTACCAACCACAGGAGCTGTGTCTCTGTAGAGAACAGCAACTC	1442
Db	938	CACACAAAGGGAGCCGCTCTCAACCCACAGGAGCTTGCTCTCTCTAGAGAGGTGACAATTC	997
Oy	1443	TAAACTGTCCCCAGAGAGGAGACTTTGAATGAGAAAACCAACACTTTGGAAGCCAAAATC	1502
Db	998	AAAACTCATCCCCAGAGAGGAGACTTGAACGAGGAA-----ACTGCGAGAAACCAAAAGTC	1051
Oy	1503	CTTT--TTCCCAAAGGTCTGAAGAAAAAAAAAAAAAAAACAAA	1544
Db	1052	CTTTTCCCCCANAAGGTTCTGAAGNAACAAACAAAACAAAACA	1094

RESULT 5	917 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AR088290			
DEFINITION	Sequence 1 from patent US 5989866.			
ACCESSION	AR088290			
VERSION	AR088290.1	GI:10015053		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 917) Delsher,T.A., Conklin,D.C., Raymond,F., Bukowski,T.R., Holdeman,S.D., Hansen,B. and Sheppard,P.O.			
TITLE	ECF homologs			
JOURNAL	Patent: US 5989866-A 1 23-NOV-1999;			
FEATURES	Location/Qualifiers 1..917			
BASE COUNT	244 a 258 c 252 g 163 t			
ORIGIN	/organism="unknown"			
Query Match	51.3%; Score 805.2; DB 6; Length 917;			
Best Local Similarity	91.6%; Pred. No. 2,3e-122;			
Matches 907; Conservative 0; Mismatches 3; Indels 80; Gaps 2;				
QY 550	ATGATTCAGCGCCCTCCGCTGACATTGCTTACACTTCCTGCTGCTTC	609		
Db 1	ATGATTCAGCGCCCTCCGCTGACATTGCTTACACTTCCTGCTGCTTC	60		
QY 610	CAGTACAGGTGCTGTTGCCGAGAGAACGTGGACTTCGCCATCCACGTGAGAACCG	669		
Db 61	CAGTACAGGTGCTGTTGCCGAGAGAACGTGGACTTCGCCATCCACGTGAGAACCG	120		
QY 670	ACGGGGGCTCGGGACGATGTAGCGCTAGCAGGTGGGGCTGTACACAGCTCTACAGCGG	729		
Db 121	ACGGGGGCTCGGGACGATGTAGCGCTAGCAGGTGGGGCTGTACACAGCTCTACAGCGG	180		
QY 730	ACCAAGTGGGAACAATCCAGAGTCTTGGGCGCAGAGATCACTGCTGCCGCGGAGAGATGG	789		
Db 181	ACCAAGTGGGAACAATCCAGAGTCTTGGGCGCAGAGATCACTGCTGCCGCGGAGAGATGG	240		
QY 790	GACAAGTATGCCCACTCTTATGTGGAGACACACACTTCGCTAGTCAATCCGATCAAG	849		
Db 241	GACAAGTATGCCCACTCTTATGTGGAGACACACACTTCGCTAGTCAATCCGATCAAG	300		
QY 850	GGCAAGGAGAGGAATCTACTGTGATGAACGCCAAGGCAAGCTGTGGGGAAGGCC	909		
Db 301	GGCAAGGAGAGGAATCTACTGTGATGAACGCCAAGGCAAGCTGTGGGGAAGGCC	360		
QY 910	GATGGACACACAGAGAGTGTCTTATCAGAGAAGTTCTGGAGAACACTACAGGCC	969		
Db 361	GATGGACACACAGAGAGTGTCTTATCAGAGAAGTTCTGGAGAACACTACAGGCC	420		
QY 970	CTGATGTGGCTATGATCTCCGGCTGTACGTGGGCTTACCAAGAAAGGGCGCGCGG	1029		

|||||
Db 421 CTGATGTCGGCTAAGTACTCCGGCTGTAGTGGGCTTCAACCAAGAGGGCGCGCG 480
QY 1030 AAGGGCCCCAAGACCCGGGAGAACCCAGACAGCTGCATTTCATGAAGGCTACCCCAAG 1089
Db 481 AAGGGCCCCAAGACCCGGGAGAACCCAGACAGCTGCATTTCATGAAGGCTACCCCAAG 540
QY 1090 GGGCAGCCGGAGCTTCAGAAAGCCCTTCAAGTACAGCAAGGCTGACCAAGAGTCCCGTCG 1149
Db 541 GGGCAGCCGGAGCTTCAGAAAGCCCTTCAAGTACAGCAAGGCTGACCAAGAGTCCCGTCG 600
QY 1150 ATCCGGGCCACACACCCCTGCTAGGCGACCCCGCGGCGCCCTCAGAGTCCCGTCGCA 1209
Db 601 ATCCGGGCCACACACCCCTGCTAGGCGACCCCGCGGCGCCCTCAGAGTCCCGTCGCA 659
QY 1210 CACTCACTCCCGAAGAACTGCATCAGAGATATTTTACATGAAGAAATGAAGAA 1269
Db 660 CACTCACTCCCGAAGAACTGCATCAGAGATATTTTACATGAAGAAATGAAGAA 708
QY 1270 GCTCTATTTTGTACATGTTGTTTAAAGAAACAAAACTGAACCAAACTCTTGGGG 1329
Db 709 ----- 708
QY 1330 GAGGGGTGAATGAATTTTATTTGCTTGAATCCCGGATGACAAAGACTCAGCGAA 1389
Db 709 -----ATAAGATTTTATTTGCTTGAATCCCGGATGACAAAGACTCAGCGAA 760
QY 1390 AAGGACTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACAGACACTTAAC 1449
Db 761 AAGGACTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACAGACACTTAAC 820
QY 1450 GTCCCCAGAGAGGAGCTTGAATGAGAAACCAACACTTTGAGAAGCCAAAGTCCCTTTTC 1509
Db 821 GTCCCCAGAGAGGAGCTTGAATGAGAAACCAACACTTTGAGAAGCCAAAGTCCCTTTTC 880
QY 1510 CCAAGGTCTGTGAAGAAAGAAAGAAAGAAAGAA 1539
Db 881 CCAAGGTCTGTGAAGAAAGAAAGAAAGAAAGAAAGAA 910

RESULT 6
AR198548
LOCUS AR198548 917 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6352971.
ACCESSION AR198548
VERSION AR198548.1 GI:20248397
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 917)
DeJsher,T.A., Conklin,D.C., Raymond,F., Bukowski,T.R.,
Holderman,S.D., Hansen,B. and Sheppard,P.O.
TITLE FGF Homologs
JOURNAL Patent: US 6352971-A 1 05-MAR-2002;
FEATURES
source Location/Qualifiers
1..917
/organism="unknown"
BASE COUNT 244 a 258 c 252 g 163 t
ORIGIN

Query Match 51.3%; Score 805.2; DB 6; Length 917;
Best Local Similarity 91.6%; Pred. No. 2,3e-122;
Matches 907; Conservative 0; Mismatches 3; Indels 80; Gaps 2;

QY 550 ATGTATTCAGCGCCCTCGGCTGCACTGCTGTGTTACACTTCTGCTGTGCTTC 609
Db 1 ATGTATTCAGCGCCCTCGGCTGCACTGCTGTGTTACACTTCTGCTGTGCTTC 60
QY 610 CAGGTACAGGCTGCTGTCGAGAGAACTGAGACTTCCGATCCAGGTGAGAACAG 669
Db 61 CAGGTACAGGCTGCTGTCGAGAGAACTGAGACTTCCGATCCAGGTGAGAACAG 120

QY 670 ACGCGGCTCGGGACGATGTAGCCGCTAAGCAGCTCGGCTTACCAGCTCTACACCGG 729
Db 121 ACGCGGCTCGGGACGATGTAGCCGCTAAGCAGCTCGGCTTACCAGCTCTACACCGG 180
QY 730 ACCAGTGGGAACATATCCAGGTCTGCGCCGAGATCAGTCCCGCGGAGATGG 789
Db 181 ACCAGTGGGAACATATCCAGGTCTGCGCCGAGATCAGTCCCGCGGAGATGG 240
QY 790 GACAGTATGCCAGCTCCAGTGTGAGACAGACACTTGGTGTGAAGTCCGATCAAG 849
Db 241 GACAGTATGCCAGCTCCAGTGTGAGACAGACACTTGGTGTGAAGTCCGATCAAG 300
QY 850 GGCAGAGACGGAATTCATACCTGTGATGAACCCGAAAGGCAAGCTCTGGGGAAGCC 909
Db 301 GGCAGAGACGGAATTCATACCTGTGATGAACCCGAAAGGCAAGCTCTGGGGAAGCC 360
QY 910 GATGGACACAGCAAGAGTGTGTTCATCAGAGAGTCTGAGAACAACTACAGGCC 969
Db 361 GATGGACACAGCAAGAGTGTGTTCATCAGAGAGTCTGAGAACAACTACAGGCC 420
QY 970 CTGATGTCGGCTAAGTACTCCGCTGTAGTGGGCTTCAACCAAGAGGGCGCGG 1029
Db 421 CTGATGTCGGCTAAGTACTCCGCTGTAGTGGGCTTCAACCAAGAGGGCGCGG 480
QY 1030 AAGGGCCCCAAGACCCGGGAGAACCCAGAGAGTGCATTTCATGAAGGCTACCCCAAG 1089
Db 481 AAGGGCCCCAAGACCCGGGAGAACCCAGAGAGTGCATTTCATGAAGGCTACCCCAAG 540
QY 1090 GGGCAGCCGGAGCTTCAGAAAGCCCTTCAAGTACAGACAGCTGACCAAGAGTCCGTCG 1149
Db 541 GGGCAGCCGGAGCTTCAGAAAGCCCTTCAAGTACAGACAGCTGACCAAGAGTCCGTCG 600
QY 1150 ATCCGGGCCACACACCCCTGCTAGGCGACCCCGCGGCGCCCTCAGAGTCCCGTCGCA 1209
Db 601 ATCCGGGCCACACACCCCTGCTAGGCGACCCCGCGGCGCCCTCAGAGTCCCGTCGCA 659
QY 1210 CACTCACTCCCGAAGAACTGCATCAGAGATATTTTACATGAAGAAATGAAGAA 1269
Db 660 CACTCACTCCCGAAGAACTGCATCAGAGATATTTTACATGAAGAAATGAAGAA 708
QY 1270 GCTCTATTTTGTACATGTTGTTTAAAGAAACAAAACTGAACCAAACTCTTGGGG 1329
Db 709 ----- 708
QY 1330 GAGGGGTGAATGAATTTTATTTGCTTGAATCCCGGATGACAAAGACTCAGCGAA 1389
Db 709 -----ATAAGATTTTATTTGCTTGAATCCCGGATGACAAAGACTCAGCGAA 760
QY 1390 AAGGACTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACAGACACTTAAC 1449
Db 761 AAGGACTGTAGTCAACCCACAGAGTGTCTCTCTAGAGACAGACACTTAAC 820
QY 1450 GTCCCCAGAGAGGAGCTTGAATGAGAAACCAACACTTTGAGAAGCCAAAGTCCCTTTTC 1509
Db 821 GTCCCCAGAGAGGAGCTTGAATGAGAAACCAACACTTTGAGAAGCCAAAGTCCCTTTTC 880
QY 1510 CCAAGGTCTGTGAAGAAAGAAAGAAAGAAAGAA 1539
Db 881 CCAAGGTCTGTGAAGAAAGAAAGAAAGAAAGAAAGAA 910

RESULT 7
AX151107
LOCUS AX151107 917 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent W00139788.
ACCESSION AX151107
VERSION AX151107.1 GI:14533309
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 917)

AUTHORS	West, J.W.
TITLE	Methods for targeting cells that express fibroblast growth receptor-3 or-2
JOURNAL	Patent: WO 0139788-A 1 07-JUN-2001;
FEATURES	Zymogenetics, Inc. (US)
source	Location/Qualifiers
	1. .917
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
CDS	1. .624
	/note="unnamed protein product"
	/codon_start=1
	/protein_id="CACA2550.1"
	/db_xref="GI:14533310"
	/translation="MSAPASACITCLCHFLILLCQVOYLVAENVDRIHVENOTRAR
	DDVSROLRIQLTSRTSGKHIOVIGRISARGSDGKVAQLLVETPTFSQVRIKKE
	ETETELCDNNRKGKLVGKPDGTSKECVIEVLVLENNYALMSARYSGVYFTKGRPR
	KGPETLQNDVDHFMKKRYPKGPDELQPFYFTYTKRSRIRPTHPA"
BASE COUNT	244 a 258 c 252 g 163 t
ORIGIN	

Query Match	51.3%	Score 805.2	DB 6	Length 917;
Best Local Similarity	91.6%	Pred. No. 2.3e-122;		
Matches 907; Conservative	0;	Mismatches 3;	Indels 80;	Gaps 2

QY	550	ATGATTTAGAGCCCTCCGGCTGCACCTTGCCTGTTTACACTTCTCGTGGTGGCTTC	609
Db	1	ATGATTTAGAGCCCTCCGGCTGCACCTTGCCTGTTTACACTTCTCGTGGTGGCTTC	60
QY	610	CAGTTCAGAGTGTCTGGTGTGGCGAGAGAACGTGACCTTCCGCATCCAGCTGGAGAACAG	669
Db	61	CAGTTCAGAGTGTCTGGTGTGGCGAGAGAACGTGACCTTCCGCATCCAGCTGGAGAACAG	120
QY	670	ACGGGGGCTCGGGACGATGTAGCCGTTAGAGACGTGCGCGCTGTACCAGTCTACAGCCGG	729
Db	121	ACGGGGGCTCGGGACGATGTAGCCGTTAGAGACGTGCGCGCTGTACCAGTCTACAGCCGG	180
QY	730	ACCAAGTGGGAAACACATCCAGGTCCCTGGGCGCGACAGATCAGTCCCGGCGACAGATGGG	789
Db	181	ACCAAGTGGGAAACACATCCAGGTCCCTGGGCGCGACAGATCAGTCCCGGCGACAGATGGG	240
QY	790	GACAAATGTGGCCGACGCTCTAGTGGAGACACAGACACTTTCGGTGTAGTCAAGTCCGATCAG	849
Db	241	GACAAATGTGGCCGACGCTCTAGTGGAGACACAGACACTTTCGGTGTAGTCAAGTCCGATCAG	300
QY	850	GGCAAGGAGACGGAATTTCTACCTGTGCATGTAACGCCAAGGCAACCTGTGGGGAGAGCC	909
Db	301	GGCAAGGAGACGGAATTTCTACCTGTGCATGTAACGCCAAGGCAACCTGTGGGGAGAGCC	360
QY	910	GATGGCACACACAGAGAGTGTGTTCATTCGAGAAAGTTCTGGAGACACATCACAGGCC	969
Db	361	GATGGCACACACAGAGAGTGTGTTCATTCGAGAAAGTTCTGGAGACACATCACAGGCC	420
QY	970	CTGATGTGCGCTTAAGTACTCTCGGCTGGTACGTGGGCTTCACACAAAGGGGCGGCGGG	1029
Db	421	CTGATGTGCGCTTAAGTACTCTCGGCTGGTACGTGGGCTTCACACAAAGGGGCGGCGGG	480
QY	1030	AAGGGCCCCAAGACCCCGGAGAACCCAGCAGGACGTGCAATTTCTATGAAGCGCTTACCCCAAG	1089
Db	481	AAGGGCCCCAAGACCCCGGAGAACCCAGCAGGACGTGCAATTTCTATGAAGCGCTTACCCCAAG	540
QY	1090	GGGAGAGCGGAGCTTCAGAAACCTTCATCAATGTAACAGAGGTGACCAAGAAGGCCCTGGG	1149
Db	541	GGGAGAGCGGAGCTTCAGAAACCTTCATCAATGTAACAGAGGTGACCAAGAAGGCCCTGGG	600
QY	1150	ATTCGGGCCACACACACCTGTAGGCCACCCCGCGCGCCCTCAGTGGTGCCTCTGGCCA	1209
Db	601	ATTCGGGCCACACACACCTGTAGGCCACCCCGCGCGCG - CCCTCAGGTGCGCCTGGCCA	659
QY	1210	CACATCACATCCCGAAGAAACATGCATCAGAGGAATATTTTACATGAAAAAATTAAGAGAGAA	1269
Db	660	CACATCACATCCCGAAGAAACATGCATCAGAGGAATATTTTTCATGAAAAA-----	708

Qy	1270	GCTCTATTTTGTGACATTTGGT	TTAAAGAGACAAAACTGACCAAACTCTGGGG	1322
Db	709	-----	-----	708
Qy	1330	GAGGGTGATAAAGATTATTTATG	CTTGAAACCCCGATGACAAAGACTCAGCA	1388
Db	709	-----	ATAGAGATTTTGTGTGACTTGAAACCCCGATGACAAAGACTCAGCA	760
Qy	1380	AGGACGTGTAGTCAACCCACAGT	GCTGCTCTCTCTGGAACGACACACTCTAACTC	1448
Db	761	AGGACGTGTAGTCAACCCACAGT	GCTGCTCTCTGGAACGACACACTCTAACTC	820
Qy	1450	GTCCCCAGAGAGAGACTTGAAT	GAGAAAACAACATTGAGAAAGCCAAAGCTCTTTTC	1509
Db	821	GTCCCCAGAGAGAGACTTGAAT	GAGAAAACAACACTTTGAGAAACCAAGCTCTTTTC	880
Qy	1510	CCAAAGGTTCTGAAAGCAAAAAA	AAAAA 1539	
Db	881	CCAAAGGTTCTGAAAAAAA	AAAAA 910	

	917 bp	DNA	linear	PAT 31-QAN-2002
BD008427				
LOCUS				
RESULT 8				
BD008427				

DEFINITION	Fibroblast growth factor homologs.
ACCESSION	BD008427
VERSION	BD008427.1 GI:18636800
KEYWORDS	JP 2001502178-A/1.
SOURCE	unidentified.

ORGANISM	REFERENCE	AUTHORS
unidentified unclassified.	1 (bases 1 to 917)	Deister, ¹ T.A., Conklin,D.C., Raymond ² ,F.C., Bukowski,T.R., Holderman,S.D., Hansen,B. and Sheppard,P.O.

TITLE	Fibroblast growth factor homologs
JOURNAL	Patent: JP 2001502178-A 1 20-FEB-2001;
COMMENT	ZYMOGENETICS INC
OS	Unidentified
PN	JP 2001502178-A/1

PD 20-FEB-2001
PF 16-OCT-1997 JP 1998518577
PR 16-OCT-1996 US 60/02646
PI THERESA A DEISHER, DARRELL C CONKLIN, PENNELA C RAYMOND, PI
THOMAS R BUKOWSKI,

	Location/Qualifiers
PI	SUSAN D HOLDERMAN, BRIGIT HANSEN, PAUL O SHEPARD PC
C12N5/18, C07K14/50, C07K16/22, C07K13/00, C12N5/10, A61K38/18	CC
Strandedness:	Double;
CC	Topology: Linear;
FH	Key

```

FT source 1..917 /organism='unidentified'.
FT Location/Qualifiers
source 1..917 /organism='unidentified'
FEATURES

```

BASE COUNT	244	a	258	c	252	g	163	t
ORIGIN	/db_xref="taxon:32644"							
Query Match	51.3%; Score 805.2; DB 6; Length 917;							

Best Local Similarity 91.68; Pred. No. 2.38-122;
Matches 907; Conservative 0; Mismatches 3; Indels 80; Gaps 2;
OY 550 ATGTAATTCAGCGCCCTCGCGCTGCACATTCCTGATTTACATTCCTGCTCTGCTTC 609
|||||

[illegible]

Qy 670 ACAGGGGCTCGSGACGATGTAGCGCTTAAGCAGCGTCGGGGCGTGTACCAGCTTTACAGCCGG 729
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 ACAGGGGCTCGSGACGATGTAGCGCTTAAGCAGCGTCGGGGCGTGTACCAGCTTTACAGCCGG 180

730 ACCAGTGGGAAACACATCCAGTCTCTGGGCCGAGATCAGTCCCGCGCGGATGGG 789
181 ACCAGTGGGAAACACATCCAGTCTCTGGGCCGAGATCAGTCCCGCGCGGATGGG 240
790 GACAAATATGCCAGTCTCTAGTGAAGACACACCTTGGTGAATCAAGTCCGATCAAG 849
241 GACAAATATGCCAGTCTCTAGTGAAGACACACCTTGGTGAATCAAGTCCGATCAAG 300
850 GGCAGAGAGAGAGAAATTCATCTGATGAACCGGAAAGCACTCTGGGGAAGCC 909
301 GGCAGAGAGAGAGAAATTCATCTGATGAACCGGAAAGCACTCTGGGGAAGCC 360
910 GATGGACACAGAGAGAGTGTGTTCATCGAAGAGTCTTGAGAACAACTACAGGCG 969
361 GATGGACACAGAGAGAGTGTGTTCATCGAAGAGTCTTGAGAACAACTACAGGCG 420
970 CTGATGTGGCTTAAGTACTCCGCGTGTGTAAGTGGCTTACCAGAGGGCGCGCGG 1029
421 CTGATGTGGCTTAAGTACTCCGCGTGTGTAAGTGGCTTACCAGAGGGCGCGCGG 480
1030 AAGGGGCCCAAGACCGGGAGAACAGAGAGTGTGATGAAAGGCTACCCCAAG 1089
481 AAGGGGCCCAAGACCGGGAGAACAGAGAGTGTGATGAAAGGCTACCCCAAG 540
1090 GGGCAGCGGAGCTTCAGAAAGCCCTTCAAGTACAGAGCGGTGACAGAGAGTCCCGTCCG 1149
541 GGGCAGCGGAGCTTCAGAAAGCCCTTCAAGTACAGAGCGGTGACAGAGAGTCCCGTCCG 600
1130 ATCCGGCCCAACACCCCTGCTAGGACACCCCGCGCGGCTTACGAGTCCGCTGGCCA 1209
601 ATCCGGCCCAACACCCCTGCTAGGACACCCCGCGCGG-CCCTAGAGTCCGCTGGCCA 659
1210 CACCTACACTCCCAAGAACTGATCAGAGAGTATTTTATGATAAATAAGAGAGA 1269
660 CACTACACTCCCAAGAACTGATCAGAGAGTATTTTATGATAAATAAGAGAGA 708
1270 GCTTATTTTGTACATGTTGTTTAAAGAGACAAAACTGAACCAAACTCTGGGG 1329
709 ----- 708
1330 GAGGGGTATTAAGATTTTATGTTGACTTGAACCCCGATGACAAAAAGACTCAGCAA 1389
709 -----ATAAGATTTTATGTTGACTTGAACCCCGATGACAAAAAGACTCAGCAA 760
1390 AGGAGCTGATGACACCAAGAGTGTCTCTCTAGAGAACAGAACTCTAACTC 1449
761 AGGAGCTGATGACACCAAGAGTGTCTCTCTCTAGAGAACAGAACTCTAACTC 820
1450 GTCCCAAGAGAGAGTGAATGAGAGAACCAACTTGAAGAACCAAGTCTTTTC 1509
821 GTCCCAAGAGAGAGTGAATGAGAGAACCAACTTGAAGAACCAAGTCTTTTC 880
1510 CCAAGGTTCTGAAGAGAAAAAAA 1539
881 CCAAGGTTCTGAAGAGAAAAAAA 910

RESULT 9
LOCUS AF211188 893 bp mRNA linear PRI 04-JAN-2000
DEFINITION Homo sapiens zFGF5 mRNA, complete cds.
ACCESSION AF211188
VERSION AF211188.1 GI:6665709
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS Deisher,T., Conklin,D., Raymond,F., Bukowski,T., Holderman,S.,
Hansen,B., Sheppard,P. and O'Hara,P.
TITLE Homo sapiens homologue of fibroblast growth factor

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 893)
AUTHORS Deisher,T., Conklin,D., Raymond,F., Bukowski,T., Holderman,S.,
Hansen,B., Sheppard,P. and O'Hara,P.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1999) Biomolecular Informatics, Zymogenetics,
Inc., 1201 Eastlake Ave. East, Seattle, Wa 98102, USA
FEATURES
source
1..893
/organism="Homo sapiens"
/db_xref="dbEST:AA621439"
/db_xref="taxon:9606"
/chromosome="5"
/map="5q35.3"
/clone="IMAGE:1033696"
1..624
/note="FGF-18; similar to fibroblast growth factor"
/codon_start=1
/product="zFGF5"
/protein_id="AAF22977.1"
/db_xref="gi:6665710"
/translation="MVSAPSACIQLCLHFLILGROVLYAEENVDRHVENOTBAR
DDVSRKQLRLQLSRTSGKHIVLGRIRISRGEDKRYQLVLEPTTPSSQVRIKK
ETERYLLCMNRKGLVGRPDGTSKECVFEIENVLENNYALMSAKISGMVVGFTYKGRPR
KSPKTRNQDVIHFMKRYPKGQPLQRPFTYVTKRSRIRIPHPA"
BASE COUNT 225 a 256 c 250 g 162 t
ORIGIN
Query Match 50.4%; Score 791.4; DB 9; Length 893;
Best Local Similarity 91.7%; Pred. No. 4.1e-120;
Matches 892; Conservative 0; Mismatches 1; Indels 80; Gaps 2;
OY 550 ATGTTACAGGCGCTCCGCGTGCACCTTGCTGTGTACACTTCCCTGCTGCTTC 609
DB 1 ATGTTACAGGCGCTCCGCGTGCACCTTGCTGTGTACACTTCCCTGCTGCTTC 60
OY 610 CAGGTACAGTGTCTGTTGCCGAGAGAGTGTGACTTCCCATCCAGTGAAGACAG 669
DB 61 CAGGTACAGTGTCTGTTGCCGAGAGAGTGTGACTTCCCATCCAGTGAAGACAG 120
OY 670 ACGGGGCTCGGAGCAGATGTAGACCGCTAGACAGCTGGCTGTACAGCCGG 729
DB 121 ACGGGGCTCGGAGCAGATGTAGACCGCTAGACAGCTGGCTGTACAGCCGG 180
OY 730 ACCAGTGGGAAACATCAGTCCAGTCTGGGCGCGAGATCACTGGCCGGGAGAGTGG 789
DB 181 ACCAGTGGGAAACATCAGTCCAGTCTGGGCGCGAGATCACTGGCCGGGAGAGTGG 240
OY 790 GACAAATATGCCAGTCTCTAGTGAAGACAGACACTTGGTGAATCAAGTCCGATCAAG 849
DB 241 GACAAATATGCCAGTCTCTAGTGAAGACAGACACTTGGTGAATCAAGTCCGATCAAG 300
OY 850 GGCAGAGAGAGAGTGTGTTCATCGAAGAGTCTTGAGAACAACTACAGGCG 909
DB 301 GGCAGAGAGAGAGTGTGTTCATCGAAGAGTCTTGAGAACAACTACAGGCG 360
OY 910 GATGGACACAGAGAGTGTGTTCATCGAAGAGTCTTGAGAACAACTACAGGCG 969
DB 361 GATGGACACAGAGAGTGTGTTCATCGAAGAGTCTTGAGAACAACTACAGGCG 420
OY 970 CTGATGTGGCTTAAGTACTCCGCGTGTGTAAGTGGCTTACCAGAGGGCGCGCGG 1029
DB 421 CTGATGTGGCTTAAGTACTCCGCGTGTGTAAGTGGCTTACCAGAGGGCGCGCGG 480
OY 1030 AAGGGGCCCAAGACCGGGAGAACAGAGAGTGTGATGAAAGGCTACCCCAAG 1089
DB 481 AAGGGGCCCAAGACCGGGAGAACAGAGAGTGTGATGAAAGGCTACCCCAAG 540
OY 1090 GGGCAGCGGAGCTTCAGAAAGCCCTTCAAGTACAGAGCGGTGACAGAGAGTCCCGTCCG 1149
DB 541 GGGCAGCGGAGCTTCAGAAAGCCCTTCAAGTACAGAGCGGTGACAGAGAGTCCCGTCCG 600
OY 1150 ATCCGGCCCAACACCCCTGCTAGGACACCCCGCGCGGCTTACGAGTCCGCTGGCCA 1209

Db	601	ATCCGGGCCACACACACCCCTGCCTAGGCCACCCCGCGGGC -CCCTCAGGTTCGCCCTGGGCCA	659
QY	1210	CACCTCACACTCCCGAANAACATGCATCAGAGGAAATATTTTACATGAAAAAATPAAGAAAGAA	1269
Db	660	CACCTCACACTCCCGAANAACATGCATCAGAGGAAATATTTTACATGAAAAA-----	708
QY	1270	GCTCATATTTTGTACATGTGTTTTAAAGAAGACAAAACATGAAACCAAACTCTTGGGGG	1329
Db	709	-----	708
QY	1330	GAGGGGTGATAGATTTTTTATTTGTTGACTTGAAAAACCCCGATGACAAAAAGATCAACGCA	1389
Db	709	-----ATAAGGATTTTATTTGTTGACTTGAAAAACCCCGATGACAAAAAGATCAACGCA	760
QY	1390	AGGGACTGTATCAACCCACAGGTGCTGTCTCTCTAGAAACAGAAACTCTTAAATC	1449
Db	761	AGGGACTGTATCAACCCACAGGTGCTGTCTCTCTAGAAACAGAAACTCTTAAATC	820
QY	1450	GTCGCCACAGAGAGGACTTGATGAGAAACCAACACTTTGAGAAACCCAAAGTCCCTTTTC	1509
Db	821	GTCCGCCACAGAGAGGACTTGATGAGAAACCAACACTTTGAGAAACCCAAAGTCCCTTTTC	880
QY	1510	CCAAAGTCTTGA 1522	
Db	881	CCAAAGTCTTGA 893	

RESULT 10	
ARI40196	
LOCUS	
DEFINITION	
Sequence 24 from patent US 6207442.	
ARI40196	947 bp
	DNA
	linear
	PAT 16-JUN-2001

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
ARI40196	ARI40196.1	GI:14482692	Unknown.	Unknown.	1 (bases 1 to 947)	Raymond,C.K.	Plasmid construction by homologous recombination	Patent: US 6207442-A 24 27-MAR-2001;	Location/Qualifiers 1..947	246 a 258 c 256 g 163 t 24 others	/'organism="unknown"

Query Match	48.7%	Score 765.2;	DB 6;	Length 947;
Best Local Similarity	88.9%;	Pred. No. 8.2e-116;		
Matches 907;	Conservative	0;	Mismatches 3;	Indels 110;
				Gaps 3;

QY	550	ATGATTTACGCGCCCTCCGCTGCACCTTGTCCTGTATTACACTTCCCTGCTGTGCTTC	609
Db	1	ATGATTTACGCGCCCTCCGCTGCACCTTGTCCTGTATTACACTTCCCTGCTGTGCTTC	60
QY	610	CAGGTACAGGTGTGTTGGCGGAGAGAACTGGACTTCGCATCTCAGTGGAGAACAG	669
Db	61	CAGGTACAGGTGTGTTGGCGGAGAGAACTGGACTTCGCATCTCAGTGGAGAACAG	120
QY	670	ACGCGGGCTCGGGAACGATGTGAGCCGTAAAGCAGCTCGGGCTGTACACACTCTACAGCCGG	729
Db	121	ACGCGGGCTCGGGAACGATGTGAGCCGTAAAGCAGCTCGGGCTGTACACACTCTACAGCCGG	180
QY	730	ACCAAGTGGAAACAATCTCAGTCTCTGGGCGCGAAGATCAGTATGCCCCGGGAGAGATGGG	789
Db	181	ACCAAGTGGAAACAATCTCAGTCTCTGGGCGCGAAGATCAGTATGCCCCGGGAGAGATGGG	240
QY	790	GACAAGTATGCCCGAAGTCTCTAGTGGAGCAACAACACTTCGCTAGTCAAGTCCGATCAAG	849
Db	241	GACAAGTATGCCCGAAGTCTCTAGTGGAGCAACAACACTTCGCTAGTCAAGTCCGATCAAG	300
QY	850	GCGAAGGAGACGAATTTACTCTGTGCAATGAACCGCAAAAGCGCAAGCTGTGTGGGGAAGCCC	909

Db	301	GGCAAGGAGACGGAATTTCTACCTGTGCATGAACCGAAGGCAAGCTCTGGGGAGAGCC	360
QY	910	GATGGCACACAGCAAGAGTGTGTTCATATCGAAGAGTTCGTGAGAACAACTACACGGCC	969
Db	361	GATGGCACACAGCAAGAGTGTGTTCATATCGAAGAGTTCGTGAGAACAACTACACGGCC	420
QY	970	CTGATGTGCGGTAACTACTCCGGGCTGGTACGTGGCCTTCACCAGAAAGGGGCGCGCGG	1029
Db	421	CTGATGTGCGGTAACTACTCCGGGCTGGTACGTGGGCTTCACCAGAAAGGGGCGCGCGG	480
QY	1030	AAGGGCCCCAGAACCCCGGGAGAACCCAGCAGACGACGACGTGCATTTATATGAAGGCTACCCCAAG	1089
Db	481	AAGGGCCCCAAACCCCGGGAGAACCCAGCAGCAGTGCATTTATATGAAGGCTACCCCAAG	540
QY	1090	GGGCGACCGGAGACTTCAGAAAGCCCTTCAAGTACACAGCAGTGATACCAAGAGTGCCCGTCGG	1149
Db	541	GGGCGACCGGAGACTTCAGAAAGCCCTTCAAGTACACAGCAGTGATACCAAGAGTGCCCGTCGG	600
QY	1150	ATCCGGCCACACACACCTGTGCCTAG-----GCCACC	1179
Db	601	ATCCGGCCACACACACCTGTGCCCTAGHRANHRYSRGNRGRGNRGNHRNRSRNNAGCACACC	660
QY	1180	CCGCCCGCGGCCCTTAGTTCGCCCTTGCGGCACACTACACTCCCAAGAAACTCATATCAGAG	1239
Db	661	CCGCCCGCGG-CCTCAGAGTTCGCCCTTGCGGCACACTACACTCCCAAGAAACTCATATCAGAG	719
QY	1240	GAATATTTTTCATGAAAAAAATAGGAAGAAGTCTATTTTGTACATGTGTGTTAAAAGA	1299
Db	720	GAATATTTTTCATGAAAAA-----	738

QY	1300	AGACAAAACTGAACCAAACTCTGGGGGAGGGGGTGATTAAGGATTTTATTTGTTGACTT	1359
Db	739	-----ATAAGATTTTATTTGTTGACTT	760
QY	1360	GAACCCCCGATGACAAAAAGACTCACGCAAAAGGACTGTAGTCAACCCACAGAGTCTTGT	1419
Db	761	GAACCCCCGATGACAAAAAGACTCACGCAAAAGGACTGTAGTCAACCCACAGAGTCTTGT	820
QY	1420	CTCTCTAGGAACGACAACTCTAACTCGTCCCGACAGAGAGGACTGAAATGAGGAAAC	1479
Db	821	CTCTCTAGGAACGACAACTCTAACTCGTCCCGACAGAGAGGACTGAAATGAGGAAAC	880
QY	1480	CACACCTTTGAGAGCCAAAGTCTTTTTCCCAAAGTTCTGAAAGGAAAAAAAAAAAAA	1539
Db	881	CACACCTTTGAGAGCCAAAGTCTTTTTCCCAAAGTTCTGAAAGGAAAAAAAAAAAAA	940

RESULT	11		
LOCUS	AX151109		
DEFINITION	AX151109	1023 bp	DNA
ACCESSION	AX151109	Sequence 3 from Patent WO0139788.	linear
VERSION	AX151109.1		PAT 22-JUN-2001
KEYWORDS	GI:14533311		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1023)		
AUTHORS	West,J.W.		
TITLE	Methods for targeting cells that express fibroblast growth		
JOURNAL	receptor-3 or-2		
	Patent: WO 0139788-A 3 07-JUN-2001;		
	ZymoGenetics, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..1023		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	1..624		
CDS	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAC42551.1"		

```

/db_xref="GI:14533312"
/translation="MYSAPSACGICLHLLICQVOVLAAENVDFRIVENOTRAR
DVSRSQRLRIYOLYSPRSGKHIOYIGRIARGDGGKYNOLYETPTFSSQAIKRS
ETBYELCMNRKGLVGRPDSTSECVYIEVLNNTALMSAKISGMYVSTTKGRPR
KGFRTENQDDVHEMKRIPRGQSELOLPYITVYTKRSRIPTPHG"
BASE COUNT      321 a      253 c      262 g      187 t
ORIGIN

```

Query Match	47.0%;	Score 737.6;	DB 6;	Length 1023;
Best Local Similarity	86.6%;	Pred. No. 2.7e-111;		
Matches 885; Conservative	0;	Mismatches 99;	Indels 38;	Gaps 5;

OY 550 ATGTTATAGAGCCCGCCCGCCGCACTTCCCGTGTGTTTACACTTCTCGTCTGCTTC 609
 Db 1 ATGTTATAGCCCGCCCGCCGCTGCACCTTCCGTGTGTTTACACTTCTCTACTGTGTGCTTC 60
 OY 610 CAGGTACAGGTCCTGTGTTGCCGAGAGAAACGTGACCTTCCGATCCAGCTGGAGAACCG 669
 Db 61 CAGGTTCAAGGTTTGGCAGCCGAGAGAAATGTGACACTTCCGATCCAGCTGGAGAACCG 120
 OY 670 ACGCGGCTCGGGACGATGTGAGCCGTAAAGACGTGCGGCTGTACAGCTTACAGCCGG 729
 Db 121 ACGCGGCTCGAGATGATGTGATGCGAAAGCAGCTGCGCTTACAGCTTATAGCAGG 180
 OY 730 ACCAGTGGAAACATATCCAGGTCCTGTGGGCCGACGATATAGTCCCGCGGCGAGATGG 789
 Db 181 ACCAGTGGAAACATATTCATTAAGTCTGTGGCCCTAGAGATCAGTCCGTGGCGAGACGG 240
 OY 790 GACAAATATGCCACCTCCTTAGTGGAGACAGACACTTCGTGATGCAAGTCCGATACAG 849
 Db 241 GACAAATATGCCACCTCCTAOTGGAGACAGATACCTTCCGGAATCAGTCCGGAATCAG 300
 OY 850 GGCAGGAGACGGAATTTCACTGTGCATGAACCGCAAAAGCAGCTGTGGGGAAGCC 909
 Db 301 GGCAGGAGACAGAAATTTCACTGTGTATGAACCGAAAGCAGCACTGTGGGGAAGCCT 360
 OY 910 GATGCACACAGAAAGAGTGTGTTCATTCAGGAAGTTCGTGGAAACACTACAGGCC 969
 Db 361 GATGTACTTAGCAAGAGATGCGTGTTCATTTGAAAGTTCGTGGAAACACTACAGGCC 420
 OY 970 CTGATGTGCGGTAACTACTCGGCTGTGATACGAGGCTTACCAAGAAAGGGGCGCGGG 1029
 Db 421 CTGATGTGTGCCAACTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 OY 1030 AAGGCGCCCAAGACCCGCGGAGAACCCAGCAGGACGTGATTTTCATGAAAGCGTACCCCAAG 1089
 Db 481 AAGGTCCTCCAGACCCGCGGAGAACCCAGCAGATGTACACTTCATGAAAGCGTATACCCCAAG 540
 OY 1090 GGGGAGCGCGGAGCTTCAAAACCCCTTCAAGTACACAGAGGTGACCAAGAGTCCCGTGG 1149
 Db 541 GGGAGGCGCGAGTGTCAAAAGCCCTTCAAAATACACAGTCCCAAGCCGATCCCGGCGG 600
 OY 1150 ATCGGCGCCACACACCTGCTGAGGCCACCCCGCGCGGCGCTCAGTCCGCTGGGCCA 1209
 Db 601 ATCGGCGCCACCTACACCCCGGCTAGG-----TCGCGCCA 633
 OY 1210 CACTGCACACTCCAGAAAATGCAATCAGAGGAATATTTTACATGAAAAATTAAGAAAGAA 1269
 Db 634 CACTGCACCCCCAGAGAACTACATCAGAGGAATAATTTTACATGAAAAATTAAGAAAGAA 693
 OY 1270 GCTCATATTTTGTACATGTGTTTAAAGAGACAAAAACACTGAACCAAACTCTTTGGGGG 1329
 Db 694 TCTCATATTTTGTACATGTGTTTTAAAGAGACAAAAACGAACTTAAATCTTTTGGGGG 753
 OY 1330 GAGGAGGTGATAGAGATTTTATTTGTGACTTAAACCCCGGATGACAAAAGACTCAGCAA 1389
 Db 754 GAGGAGGTGAT-AGGATTTCACTGTTTGAACCTTAA---CCCATGTACAAAAGGCTCAGCAA 809
 OY 1390 AGGAGCTGTACTCAACCCACAGGTGCTGTCTCTCTAGGACAGCAACTCTTAAATC 1449
 Db 810 GGGGAGCGCTGTCAACCCACAGGTGCTGTCTCTCTAGGAGGTGACAAATCTAAAACTC 869
 OY 1450 GTCCCCAGAGAGAGACTTTGAATGAGGAACCAACACTTTTGAAGAACCAAGTCCCTT-TT 1508

Db	870	ATCCCCAGAGGAGACTTGAACGAGAA-----ACTCGAGAAACCAAGTCTTCC	923
Qy	1509	CCCAAGGTTCTGAAGGAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA	1568
Db	924	CCCAAGGTTCTGAAGCAACAAAAAAAAAAAAAAAAAAAAA	983
Qy	1569	AA 1570	
Db	984	AA 985	

RESULT 12			
LOCUS	AF211187		
DEFINITION	Mus musculus zfcf5 mRNA, complete cds.	946 bp	Linear
ACCESSION	AF211187		
VERSION	AF211187.1	GI:6665707	
KEYWORDS			
SOURCE	Mus musculus.		
ORGANISM	Mus musculus		

REFERENCE
AUTHORS
1 (bases 1 to 946)
Deisner, T., Conklin, D., Raymond, F., Bukowski, T., Holderman, S.,
Hansen, B., Sheppard, P. and O'Hara, P.
Direct Submission
Submitted (03-DEC-1999) Biomolecular Informatics, Zymogenetics,
Inc., 1201 Eastlake Ave. East, Seattle, Wa 98102, USA
Location/Qualifiers

```

/organism="Mus musculus"
/db_xref="dbEST:AA064198"
/db_xref="taxon:10090"
/clone="IMAGE:480695"
1..624
CDS

```

```

/ncore="FGF-18; similar to fibroblast growth factor"
/coodn_start=1
/product="zFGF5"
/protein_id="AAF22976.1"
/db_xref="GI:6665708"
/translation="MYSAPSACMCICHLFLLCPOVYLAEEVNDRIHVENQTRAR
DDVSRKDLRIQLQLSRTSGKHIOVLGRISARGDGKATQMLVLEDTFSQYRIK
KIEFTYLCMNRKGLVGRAPGDTSECVETIEVLENTNTALSAVYSGVYVFETKKGRPR
KGPETRENOODVHMKRPPKGGQELQPFYVTVTKSRIRIPTHPG"
BASE COUNT      260 a      248 c      253 g      185 t

```

Query Match	44.68;	Score 700.2;	DB 10;	Length 946;
Best Local Similarity	86.28;	Pred. No. 3.7e-105;		
Matches 847; Conservative	0;	Mismatches 98;	Indels 38;	Gaps 5

QY	550	ATGATTCAGAGCCCTCGCCTGACATGACCTGGTTTACATCTTCGCTGCTGCTC	609
Db	1	ATGATTCAGAGCCCTCGCCTGACATGACCTGGTTTACATCTTCGCTGCTGCTTC	60
QY	610	CAGGTACAGTGTCGTGTTGCCGAGAGAACGTGGACTTCCGATCCAGCTGGAGAACAG	669
Db	61	CAGGTTCAGGTGTGGAGCCGAGAGAAATGTGGACTTCCGATCCAGCTGGAGAACAG	120
QY	670	ACGGGGGCTCGGACGATGTGACCCGTAAGAGCTGGGGCTGTACCAAGCTCTAACGGCGG	729
Db	121	ACGGGGGCTCGAAGTGTATGTGTGAGTCGGAGACAGCTTGCGCTTGTACCAAGCTCTAACGAGG	180
QY	730	ACCAAGTGGAAACATATCCAGAGTCTCTGGGCCGACAGATCAAGTGGCCGCGAGAGATGGG	789
Db	181	ACCAAGTGGAAAGCACAATTTAAAGTCTCTGGGCCGTAGGATCAAGTGGCCGCGAGAGACGGG	240
QY	790	GACAAAGTATGCCCAAGTCCCTAAGTGGAGAACACACACTTCGTGTAGTCAAGTCCGGATTAAG	849
Db	241	GACAAAGTATGCCCAAGTCTCTAAGTGGAGAACATATCTTCGTGGAGATCAAGTCCGGATTAAG	300
QY	850	GGCAGAGAGACGGAATTCCTACCTGTGCATACACCGCAAAAGCAAGCTCTGTGGGGAAGCCC	909

ACCESSION AC093246 GI:17921222
VERSION AC093246.3
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 175154)
DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 175154)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 175154)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE Direct Submission
AUTHORS Submitted (18-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 18, 2001 this sequence version replaced gi:15290460.
COMMENT Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.3% of Sequence;
Estimated Total Number of Errors is 1.
Location/Qualifiers
FEATURES
source 1..175154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-117L6"
BASE COUNT 47019 a 43250 c 40808 g 44077 t
ORIGIN
Query Match 41.5%; Score 651.2; DB 9; Length 175154;
Best Local Similarity 98.8%; Pred. No. 4.3e-97;
Matches 656; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 903 GAAGCCCGATGGACACGACGAGAGGTGTGTTCATCGAGAAAGTCTTGAGAAACAATA 962
DB 38537 GCGGCCGATGACGACGACGAGAGAGGTGTGTTCATCGAGAAAGTCTTGAGAAACAATA 38478
QY 963 CAGGCCCTGATGTGGCTAGTACTCCGAGTGGTGTGCTTACCAAGAGGGCG 1022
DB 38477 CAGGCCCTGATGTGGCTAGTACTCCGAGTGGTGTGCTTACCAAGAGGGCG 38418
QY 1023 GCCGCGAAGGGCCCAAGACCCGGGAGAACCAAGAGAGTGCATTTCATGAAGCGCTA 1082
DB 38417 GCCGCGAAGGGCCCAAGACCCGGGAGAACCAAGAGAGTGCATTTCATGAAGCGCTA 38358
QY 1083 CCCCCAAGGGGACCGCGAGTCTTGAAGACCTTCAAGTACAGACGCTGACCAAGAGTGC 1142
DB 38357 CCCCCAAGGGGACCGCGAGTCTTGAAGACCTTCAAGTACAGACGCTGACCAAGAGTGC 38298
QY 1143 CCGTCGATCCGGCCACACACACCTGCTTAGGCGACCCGCGCGGCGCTTCAGTGGCC 1202
DB 38297 CCGTCGATCCGGCCACACACACCTGCTTAGGCGACCCGCGCGGCGCTTCAGTGGCC 38238
QY 1203 CTGGCCACATCTACATCCAGAAAATGCATCAGAGAAATATTTTACATGAATAATA 1262
DB 38237 CTGGCCACATCTACATCCAGAAAATGCATCAGAGAAATATTTTACATGAATAATA 38178
QY 1263 GGAAGAAGCTCTATTTTGTACATTTGTGTTAAAGAGACAAATAAGTCAACCAAACTC 1322
DB 38177 GGAAGAAGCTCTATTTTGTACATTTGTGTTAAAGAGACAAATAAGTCAACCAAACTC 38118
QY 1323 TTGGGGGAGGGGTGAAGATTTTATTTGACTTGAACCCCGGATGACAAAAGACT 1382
DB 38117 TTGGGGGAGGGGTGAAGATTTTATTTGACTTGAACCCCGGATGACAAAAGACT 38058

QY 1383 CACGCAAGGAGACTGTAGTCAACCCACAGGTGCTGTCTCTCTAGGAACAGACAATC 1442
DB 38057 CACGCAAGGAGACTGTAGTCAACCCACAGGTGCTGTCTCTCTAGGAACAGACAATC 37998
QY 1443 TAAACTGTCCCAAGAGGAGACTTGAATGAGAAACCAACTTTTGAGAACCAAGTGC 1502
DB 37997 TAAACTGTCCCAAGAGGAGACTTGAATGAGAAACCAACTTTTGAGAACCAAGTGC 37938
QY 1503 CTTTTCCTCCCAAGGTTCTGAAAGAAAAAACAACAAAAAACAACAAAAAACAAGT 1562
DB 37937 CTTTTCCTCCCAAGGTTCTGAAAGAAAAAACAACAAAAAACAACAAAAAACAAGT 37878
QY 1563 AAAA 1566
DB 37877 GAAA 37874
RESULT 15
AX481447 624 bp DNA linear PAT 16-AUG-2002
LOCUS AX481447
DEFINITION Sequence 61 from Patent WO02055693.
ACCESSION AX481447
VERSION AX481447.1 GI:22316361
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 61 18-JUL-2002;
Ribopharma AG (DE)
Location/Qualifiers
FEATURES
source 1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 142 a 180 c 197 g 105 t
ORIGIN
Query Match 39.7%; Score 624; DB 6; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 550 ATGTATTCAGCGCCCTCCGCTGCACTTGCCTGTTTACACTTCCGTGCTGTCTTC 609
DB 1 ATGTATTCAGCGCCCTCCGCTGCACTTGCCTGTTTACACTTCCGTGCTGTCTTC 60
QY 610 CAGTACAGGTGCTGTGGCGAGGAAGACGTGACTCCGCATCCACGTGAGAACAG 669
DB 61 CAGTACAGGTGCTGTGGCGAGGAAGACGTGACTCCGCATCCACGTGAGAACAG 120
QY 670 ACGCGGGCTCGGAGCATGTGAGCCCTTAAGCAGCTCGGTGTACCAAGCTTACACCGG 729
DB 670 ACGCGGGCTCGGAGCATGTGAGCCCTTAAGCAGCTCGGTGTACCAAGCTTACACCGG 729
QY 121 ACGCGGGCTCGGAGCATGTGAGCCCTTAAGCAGCTCGGTGTACCAAGCTTACACCGG 180
DB 121 ACGCGGGCTCGGAGCATGTGAGCCCTTAAGCAGCTCGGTGTACCAAGCTTACACCGG 180
QY 730 ACCAGTGGGAAACATATCCAGGCTGTGGCGGAGATCAGTCCCGCGGAGATGGG 789
DB 730 ACCAGTGGGAAACATATCCAGGCTGTGGCGGAGATCAGTCCCGCGGAGATGGG 789
QY 181 ACCAGTGGGAAACATATCCAGGCTGTGGCGGAGATCAGTCCCGCGGAGATGGG 240
DB 181 ACCAGTGGGAAACATATCCAGGCTGTGGCGGAGATCAGTCCCGCGGAGATGGG 240
QY 790 GACAAATATGCCAGCTCTAGTGAAGACAGACACTTGGTAGTCAAGTCCGATCAAG 849
DB 790 GACAAATATGCCAGCTCTAGTGAAGACAGACACTTGGTAGTCAAGTCCGATCAAG 849
QY 241 GACAAATATGCCAGCTCTAGTGAAGACAGACACTTGGTAGTCAAGTCCGATCAAG 300
DB 241 GACAAATATGCCAGCTCTAGTGAAGACAGACACTTGGTAGTCAAGTCCGATCAAG 300
QY 850 GGCAGAGAGACGAAATTTCTACTGTGCTGATGAACCCGAAAGGCAAGTCTGGGGAAGCCG 909
DB 850 GGCAGAGAGACGAAATTTCTACTGTGCTGATGAACCCGAAAGGCAAGTCTGGGGAAGCCG 909
QY 301 GGCAGAGAGACGAAATTTCTACTGTGCTGATGAACCCGAAAGGCAAGTCTGGGGAAGCCG 360
DB 301 GGCAGAGAGACGAAATTTCTACTGTGCTGATGAACCCGAAAGGCAAGTCTGGGGAAGCCG 360
QY 910 GATGGCAGCAGCAAGAGTGTGTTCATGAGAAAGTCTTGGAACAACACTACACGGCC 969
DB 910 GATGGCAGCAGCAGAGAGTGTGTTCATGAGAAAGTCTTGGAACAACACTACACGGCC 969
QY 361 GATGGCAGCAGCAGAGAGTGTGTTCATGAGAAAGTCTTGGAACAACACTACACGGCC 420
DB 361 GATGGCAGCAGCAGAGAGTGTGTTCATGAGAAAGTCTTGGAACAACACTACACGGCC 420
QY 970 CTGATGTGGCTTAAGTACTCCGGCTGTGTAAGTGTGACTTGAACCCCGGATGACAAAAGACT 1029

```

Db 421 CTGATGTCGGCTAGTACTCCGGCTGTAGTGGGCTTACCAAGAGGGGGCCCGG 480
QY 1030 AAGGGCCCCAAGACCCGGGGAACACAGAGAGGTGATTTCATGAAGCGCTACCCCAAG 1089
Db 481 AAGGGCCCCAAGACCCGGGGAACACAGAGAGGTGATTTCATGAAGCGCTACCCCAAG 540
QY 1090 GGGCAGCCGAGGCTCAGAGCCCTTCAAGTACACGAGGTGACCAAGAGAGTCCCGTCGG 1149
Db 541 GGGCAGCCGAGGCTCAGAGCCCTTCAAGTACACGAGGTGACCAAGAGAGTCCCGTCGG 600
QY 1150 ATCCGGCCACACACCCCTGCTAG 1173
Db 601 ATCCGGCCACACACCCCTGCTAG 624

```

Search completed: April 26, 2003, 17:19:49
 Job time : 3148 secs

THIS PAGE BLANK (USPTO)